

FIG. 1

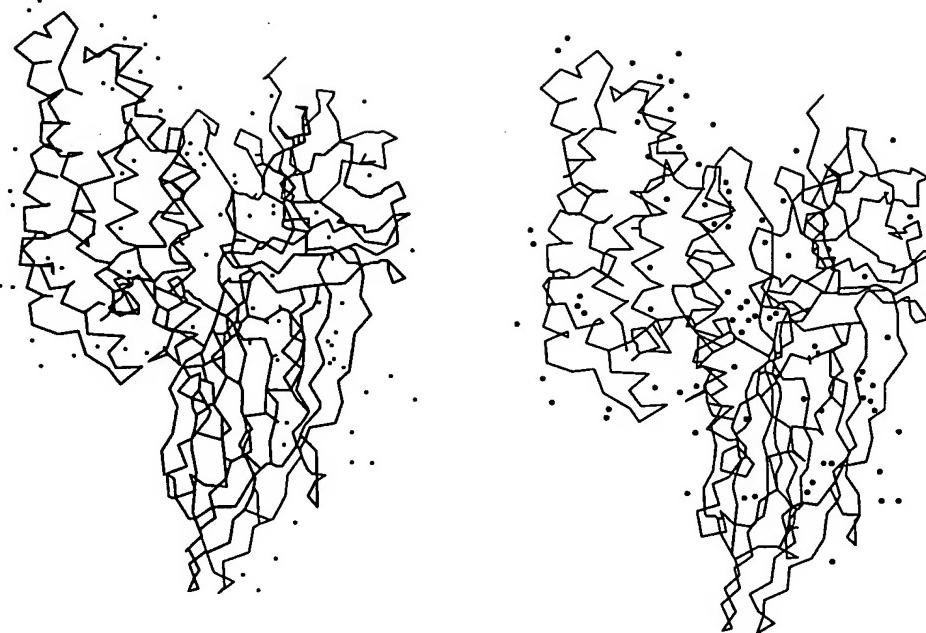


FIG. 2

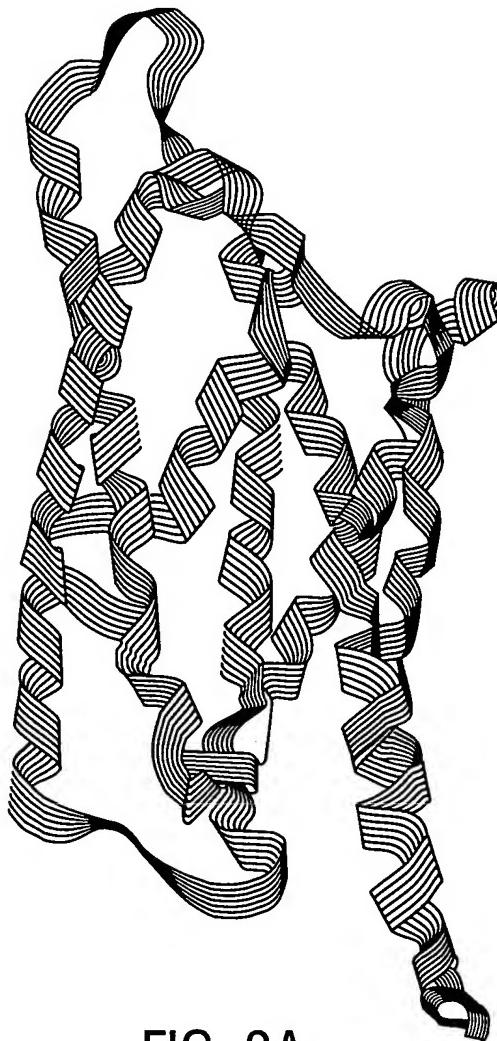


FIG. 3A

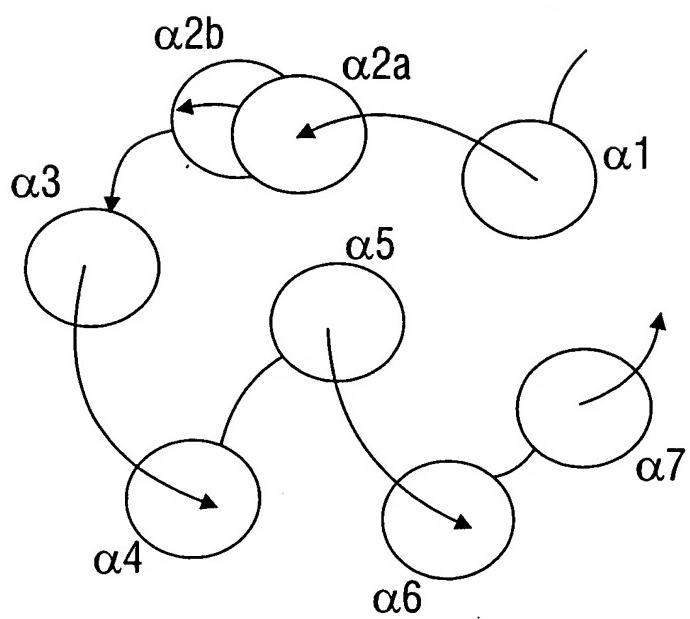


FIG. 3B

alpha helix	Amino acid Residues
$\alpha_1$	63-79
$\alpha_{2a}$	85-98
$\alpha_{2b}$	105-118
$\alpha_3$	124-153
$\alpha_4$	161-186
$\alpha_5$	194-215
$\alpha_6$	223-255
$\alpha_7$	260-286

FIG. 4

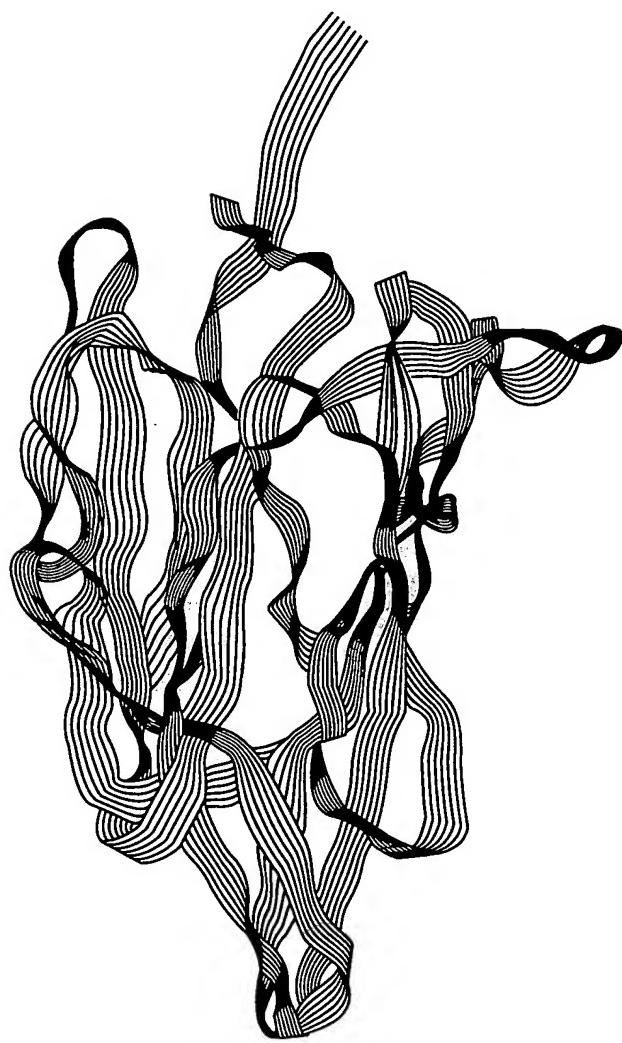


FIG. 5A

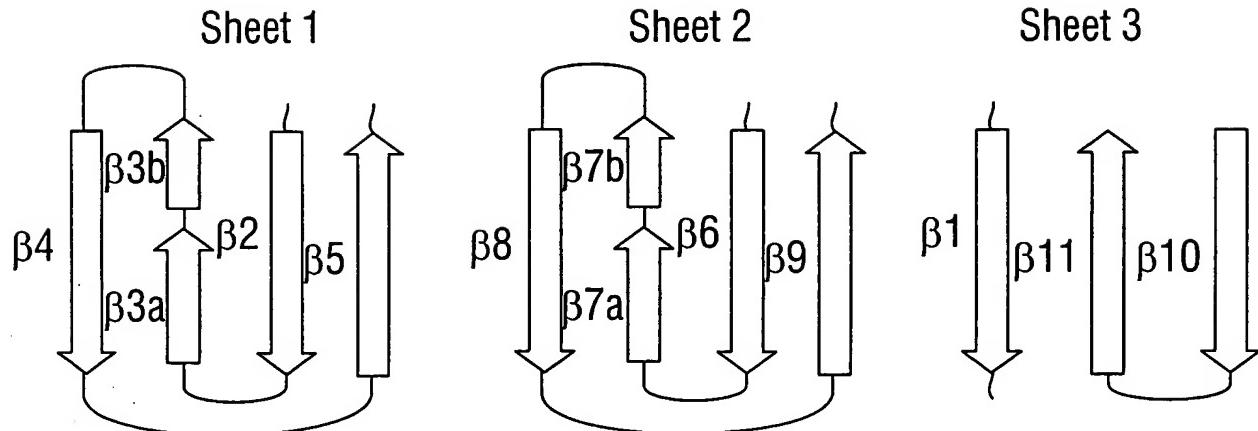


FIG. 5B

Sheet 1

$\beta$ Strand	Amino Acid Residue
$\beta_2$	339-350
$\beta_3a$	256-360
$\beta_3b$	362-368
$\beta_4$	375-379
$\beta_5$	390-395

Sheet 2

$\beta$ Strand	Amino Acid Residue
$\beta_6$	402-412
$\beta_7a$	416-419
$\beta_7b$	423-430
$\beta_8$	435-442
$\beta_9$	452-456

Sheet 3

$\beta$ Strand	Amino Acid Residue
$\beta_1$	296-306
$\beta_{10}$	472-483
$\beta_{11}$	492-498

FIG. 6

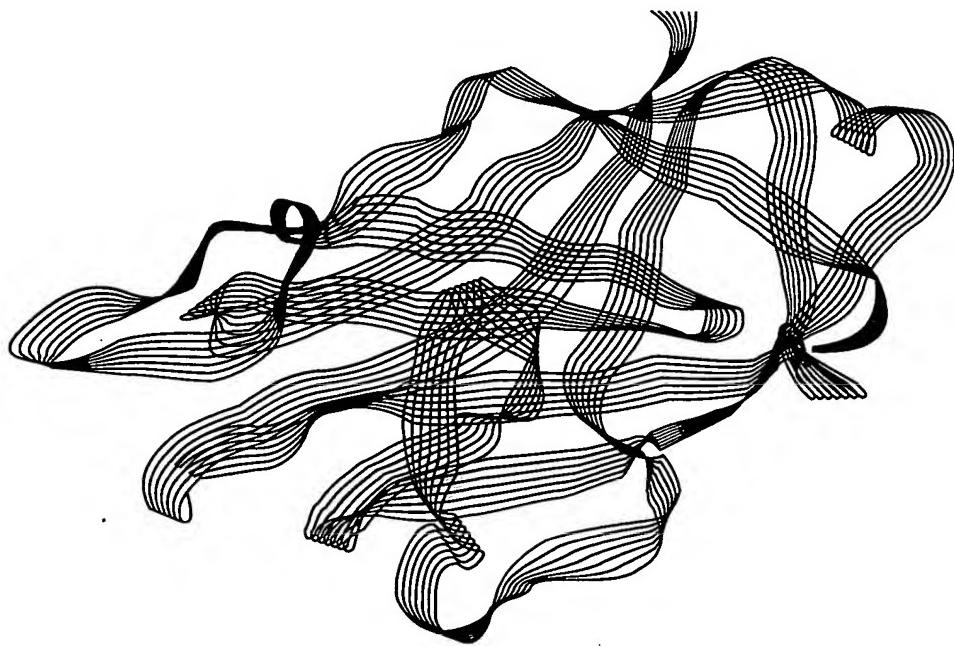


FIG. 7A

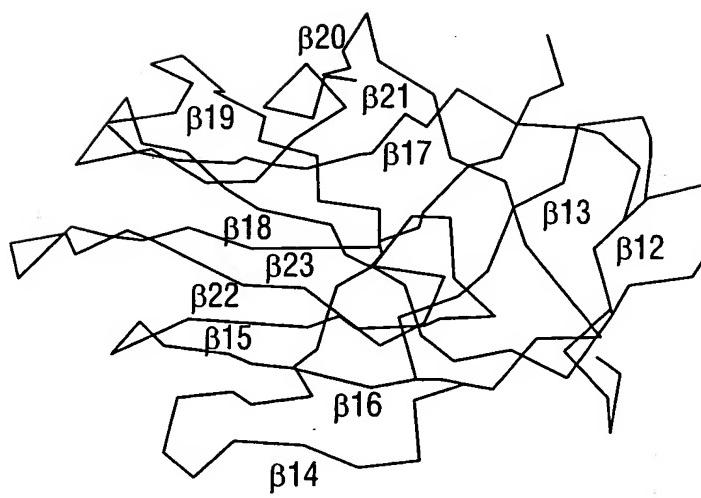


FIG. 7B

Strand Number	Amino Acid Residues
$\beta$ 12	505-509
$\beta$ 13	512-515
$\beta$ 14	522-528
$\beta$ 15	539-544
$\beta$ 16	550-557
$\beta$ 17	563-574
$\beta$ 18	578-584
$\beta$ 19	590-596
$\beta$ 20	609-614
$\beta$ 21	616-619
$\beta$ 22	626-636
$\beta$ 23	638-650

FIG. 8



FIG. 9A

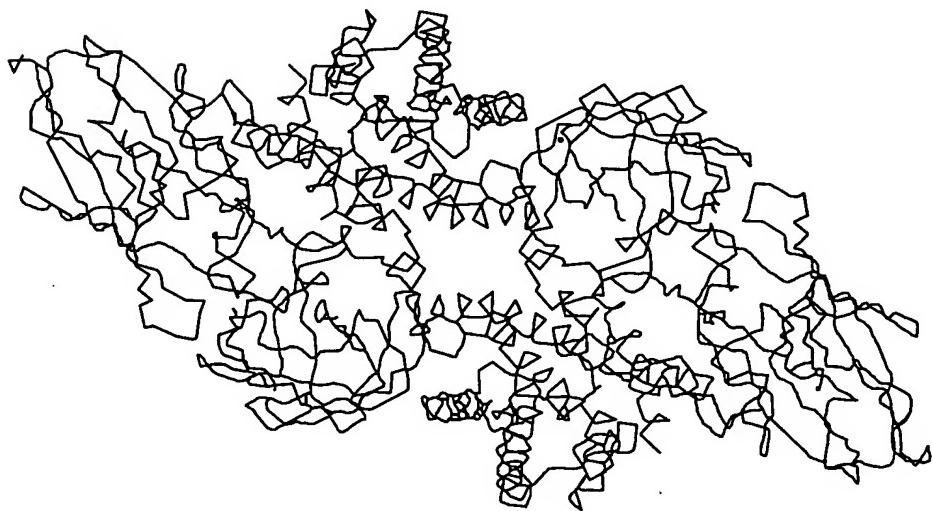


FIG. 9B

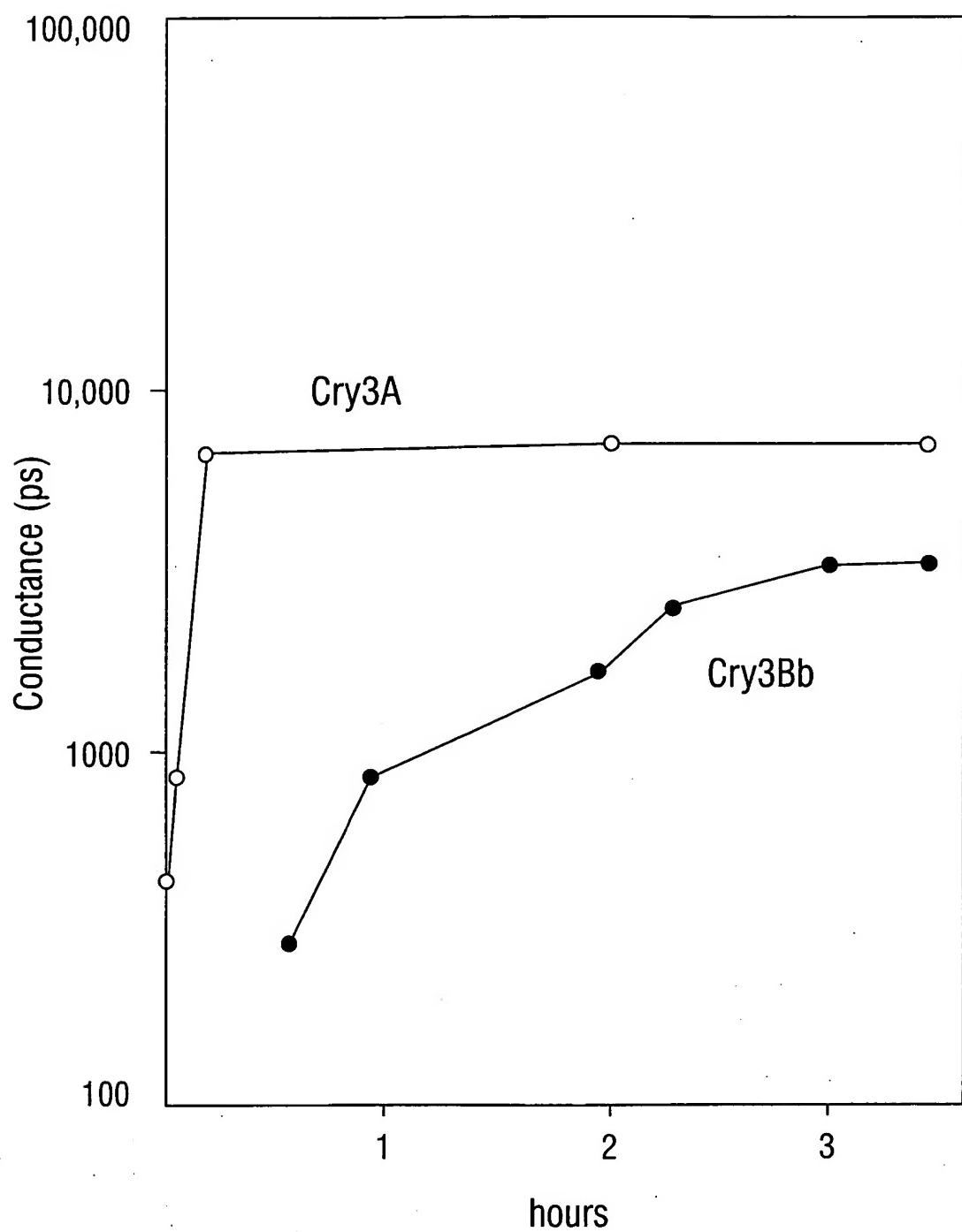


FIG. 10

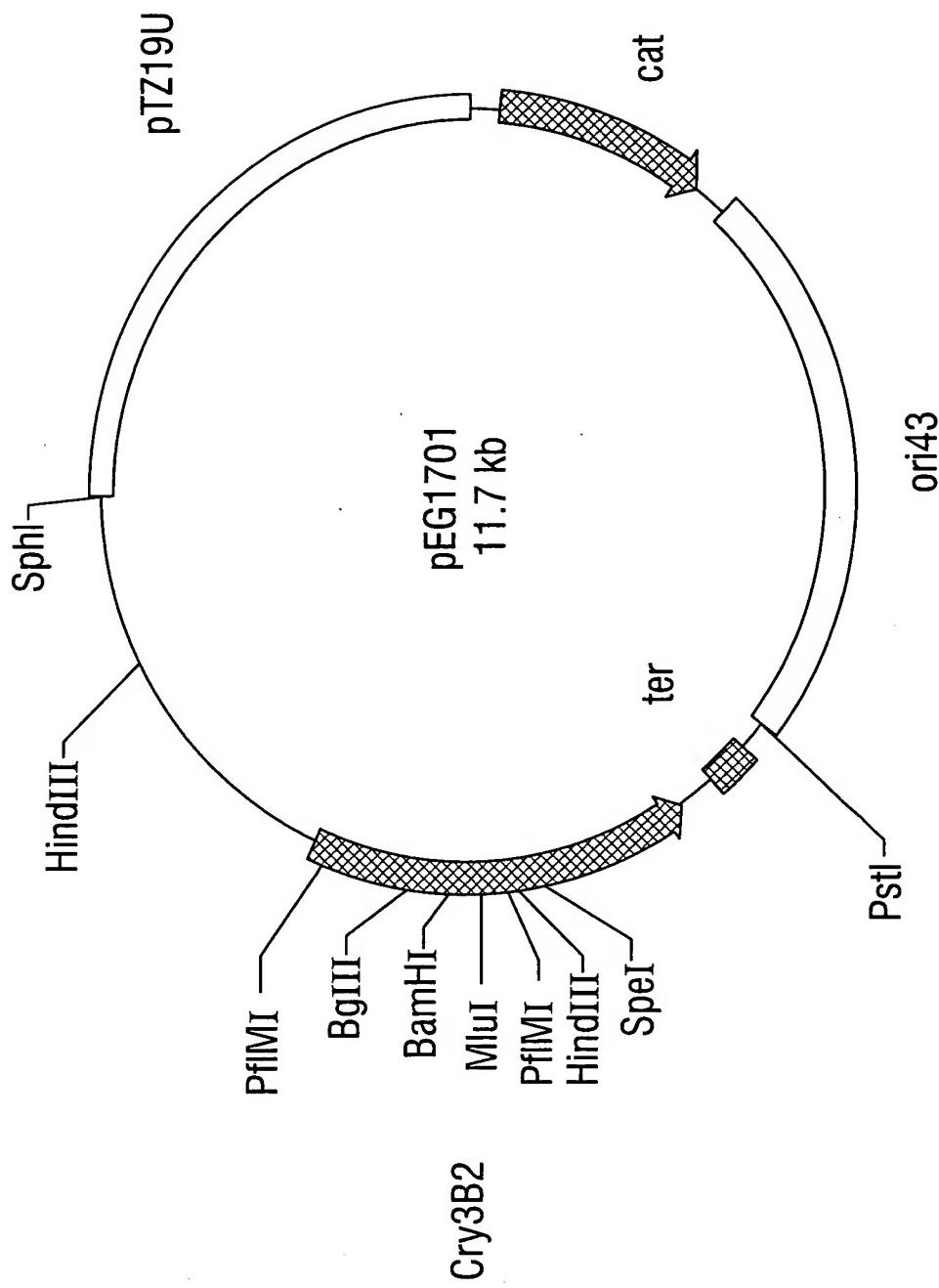


FIG. 11

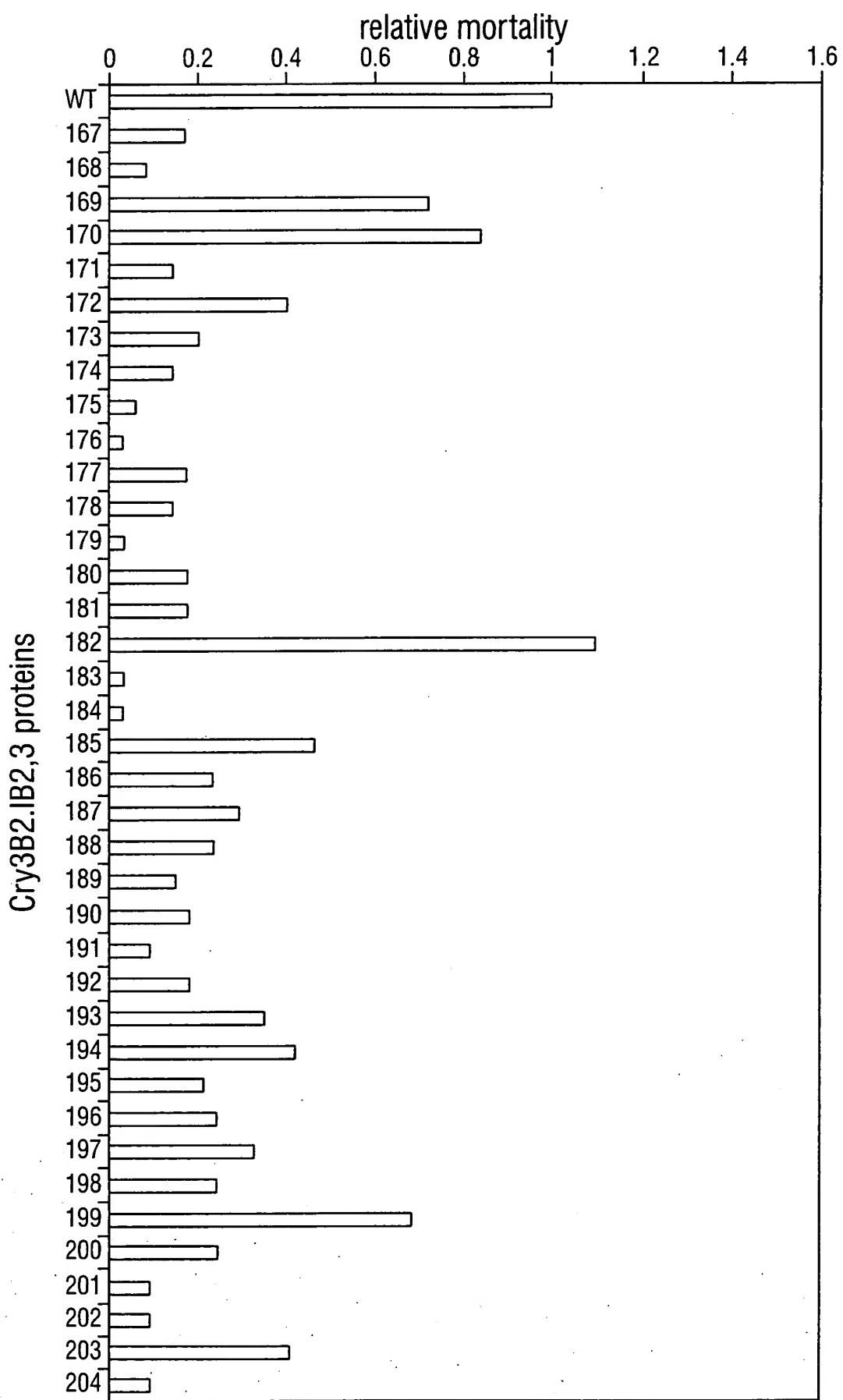


FIG. 12

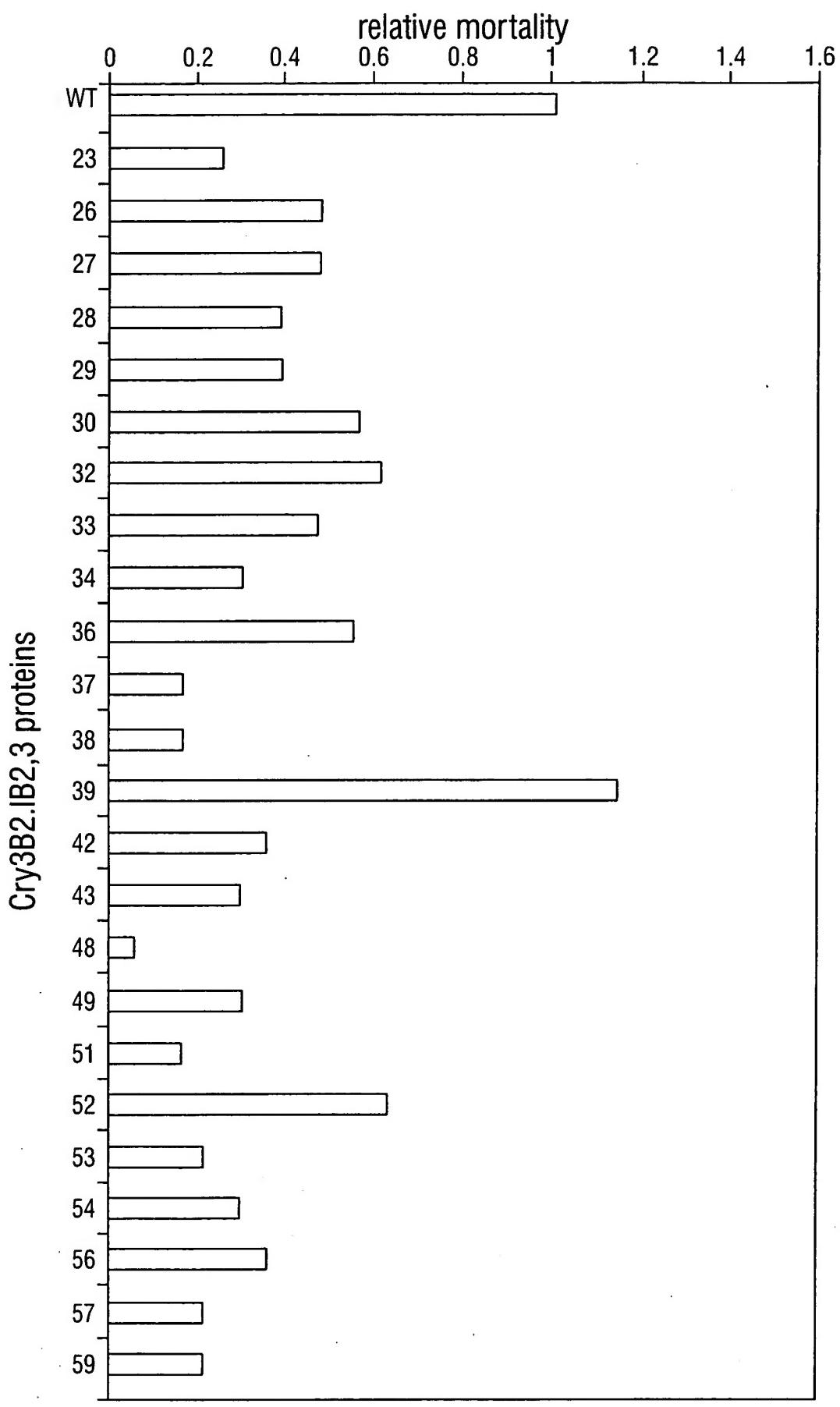


FIG. 13

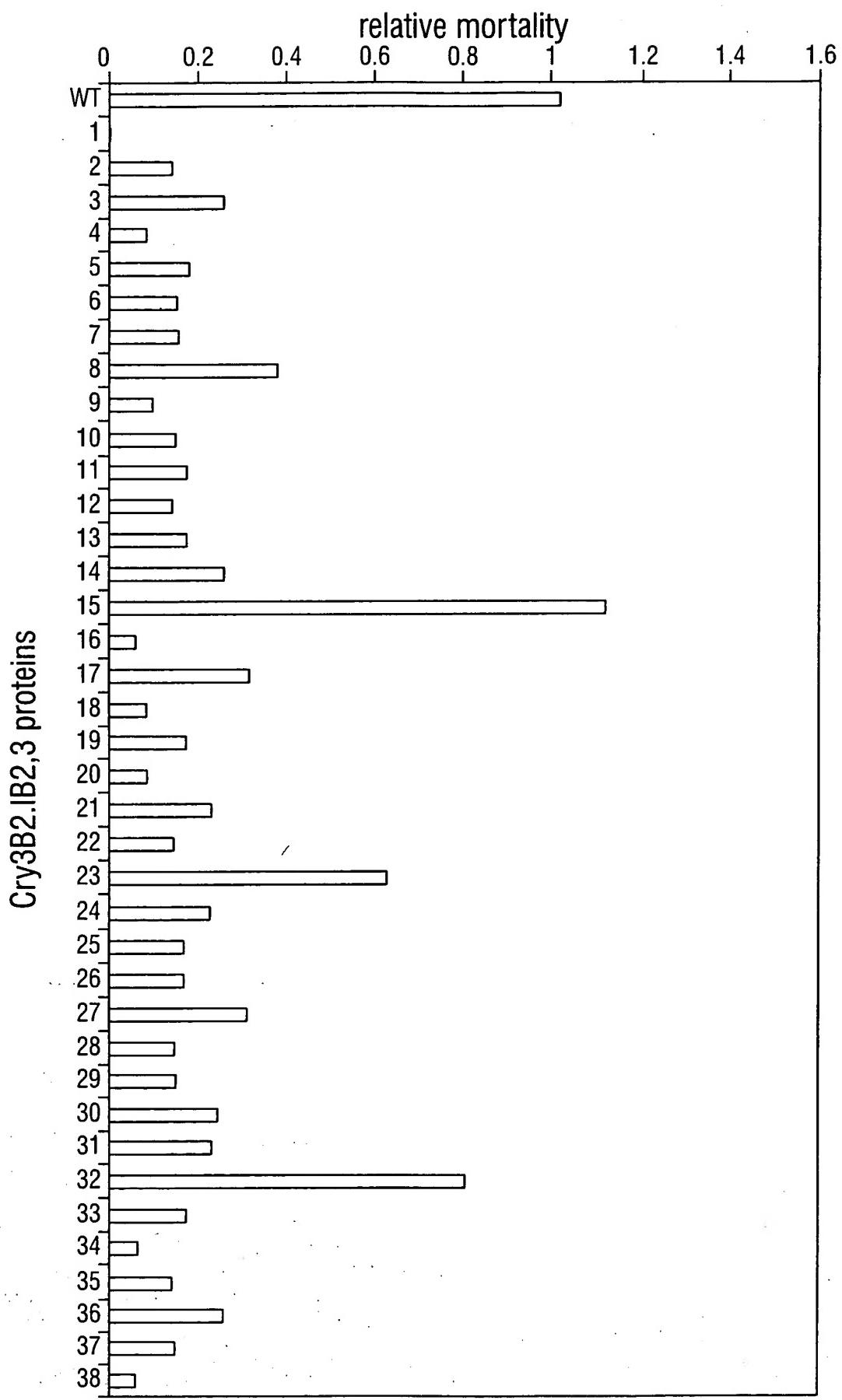


FIG. 14

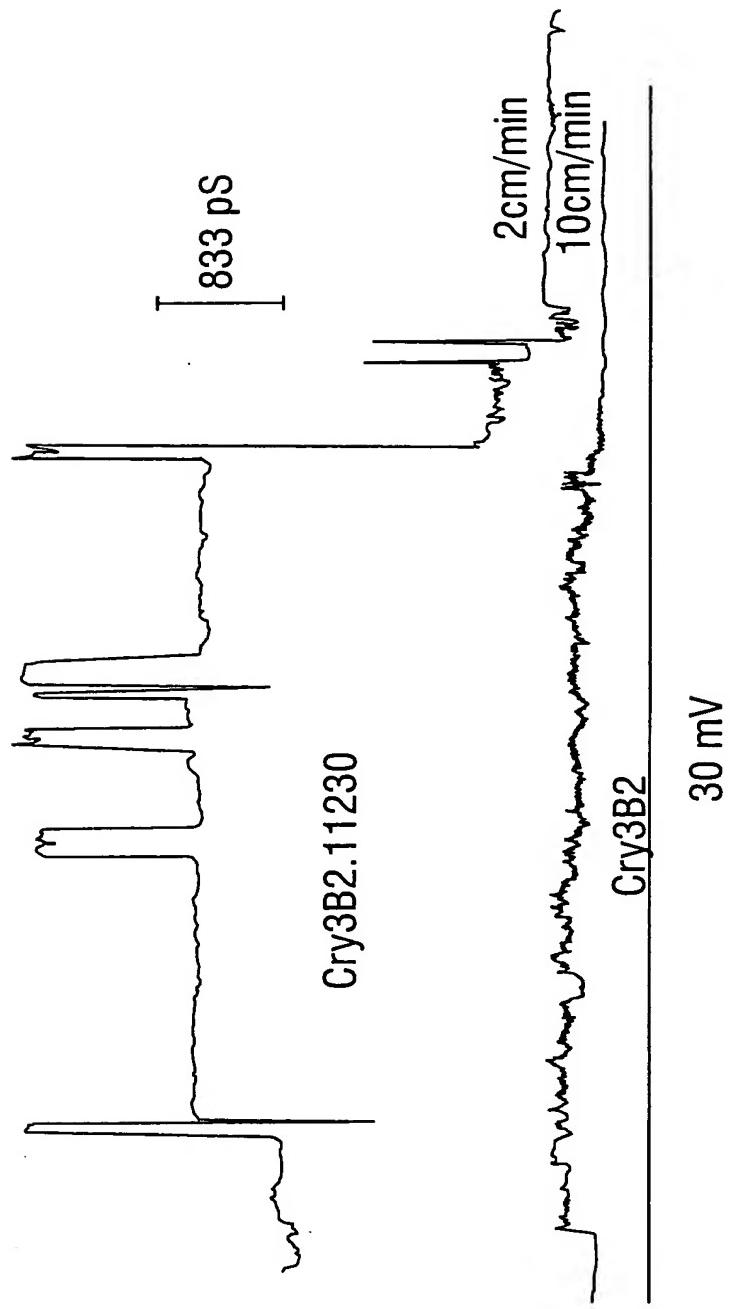


FIG. 15

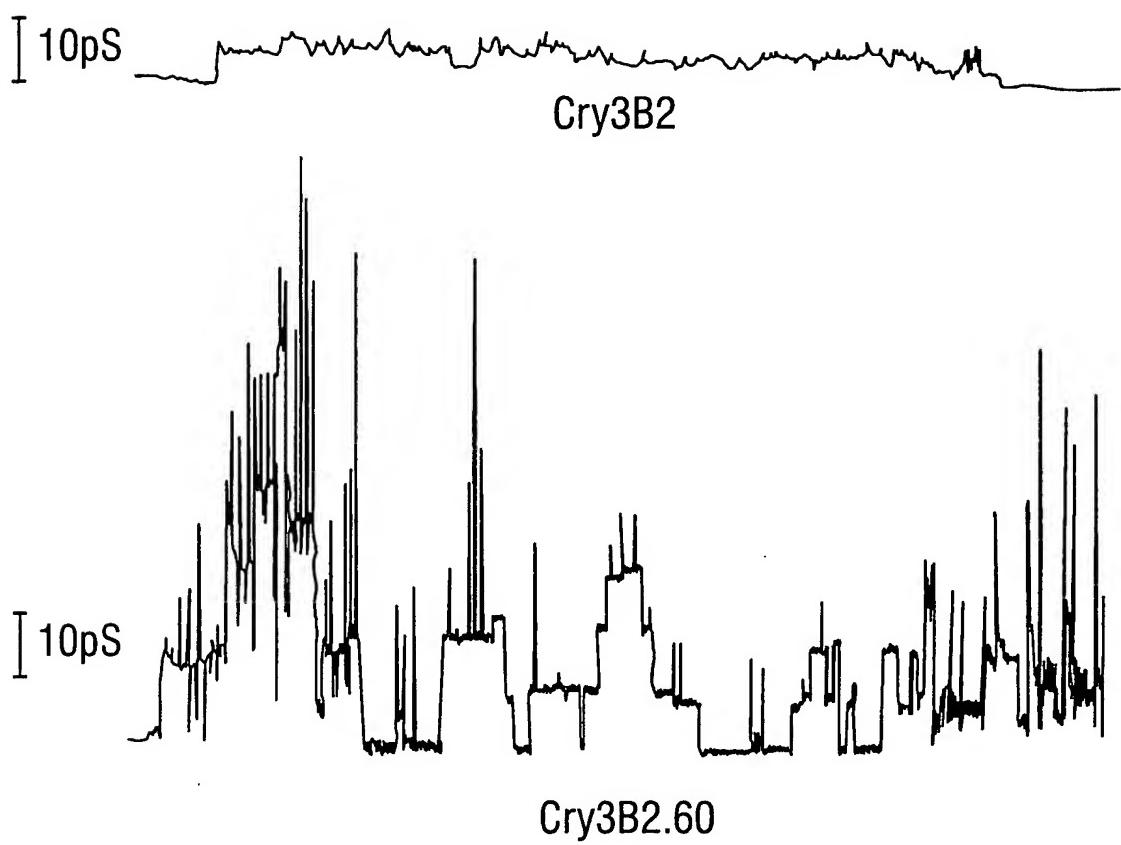


FIG. 16

## ALIGNMENT OF CRY3 SEQUENCES

(Numbered according to Cry3BB)  
(alpha helices underlined, beta sheets marked with + + +'s)

	1	10	20	30	40
CRY3C:	MNPNNRSEHDTIKATENNEVSNNHAQYPLADTP--TLEELNY				
CRYCBB2:	MNPNNRSEHDTIKVTPNSELPTNHNQYPLADNPNSTLEELNY				
CRY3BB:	MNPNNRSEHDTIKVTPNSELQTNHNQYPLADNPNSTLEELNY				
CRY3BA:	MIRMGGRKMNPNNRSEHDTIKVTPNSELPTNHNQYPLADNPNSTLEELNY				
CRY3A:	MIRKGGRKMNPNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDNY				
	50	60	70	80	90
CRY3C:	KEFLRRRTTDNNVEALDSSTTKDAIQKGISIIGDLLGVGVGFPYGGALVSFY				
CRYCBB2:	KEFLRMTEDSSTEVLDSNSTVKDAVGTGISVVGQILGVGVGPFAGALTSFY				
CRY3BB:	KEFLRMTEDSSTEVLDSNSTVKDAVGTGISVVGQILGVGVGPFAGALTSFY				
CRY3BA:	KEFLRMTADNSTEVLDSSTVKDAVGTGISVVGQILGVGVGPFAGALTSFY				
CRY3A:	KEFLRMTADNNTEALDSSTTK <u>DVIQKGISVVG</u> DLGVGVGPFGALVSFY				
	100	110	120	130	140
CRY3C:	TNLLNTIWPGE-DPLKAFMQQVEALIDQKIADYAKDKATAELQGLKNVFK				
CRY3BB2:	QSFLDTIWPSDADPKAFMAQVEVLIDKKIEEYAKSKALAELQGLQNNFE				
CRY3BB:	QSFLNTIWPSDADPKAFMAQVEVLIDKKIEEYAKSKALAELQGLQNNFE				
CRY3BA:	QSFLNAIWPSDADPKAFMAQVEVLIDKKIEEYAKSKALAELQGLQNNFE				
CRY3A:	<u>TNFLNTIWPSE-DPKAFMEQVEALMDQKIADYAKN</u> KALAELQGLQNNVE				
	150	160	170	180	190
CRY3C:	DYVSALDSWDKTPLTLRDGRSQGRIRELFSQAESHFRNSMPSFAVSGYEV				
CRY3BB2:	DYVNALNSWKKTPLSLRSKRSQDRIRELFSQAESHFRNSMPSFAVSKFEV				
CRY3BB:	DYVNALNSWKKTPLSLRSKRSQDRIRELFSQAESHFRNSMPSFAVSKFEV				
CRY3BA:	DYVNALDSWKKAPVNLRSSRQDRIRELFSQAESHFRNSMPSFAVSKFEV				
CRY3A:	<u>DYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNSMPSFAISGYEV</u>				

FIG. 17A

	200	210	220	230	240
CRY3C:	LFLPTYAQAAANTHLLLKDAQIYGTDWGYSTDDLNEFHTKQKDLTIEYTN				
CRY3BB2:	LFLPTYAQAAANTHLLLKDAQVFGEEWGYSSEDVAEFYHRQLKLTQQYTD				
CRY3BB:	LFLPTYAQAAANTHLLLKDAQVFGEEWGYSSEDVAEFYHRQLKLTQQYTD				
CRY3BA:	LFLPTYAQAAANTHLLLKDAQVFGEEWGYSSEDAEFYQRQLKLTQQYTD				
CRY3A:	<u>LFLTTYAQAAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYTD</u>				
	250	260	270	280	290
CRY3C:	HCAKWYKAGLDKLRLGSTYEEWVKFNRYRREMTLTVDLITLFPLYDVRTY				
CRY3BB2:	HCVNWYNVGLNLRLGSTYDAWVKFNRFRRREMTLTVDLIVLFPFYDVRLY				
CRY3BB:	HCVNWYNVGLNLRLGSTYDAWVKFNRFRRREMTLTVDLIVLFPFYDIRLY				
CRY3BA:	HCVNWYNVGLNSLRGSTYDAWVKFNRFRRREMTLTVDLIVLFPFYDVRLY				
CRY3A:	<u>HCVKWYNVGLDKLRLGSSYESWVNFRREMTLTVDLIALFPLYDVRLY</u>				
	300	310	320	330	340
CRY3C:	TKGVKTELTRDVLTDPIAVAVNNMNGYGTTSFSNIENYIRKPHLFDYLAHQ				
CRY3BB2:	SKGVKTELTRDIFTDPIFSNLTQEYGPTFLSIENSIRKPHLFDYLQGIE				
CRY3BB:	SKGVKTELTRDIFTDPIFSNLTQEYGPTFLSIENSIRKPHLFDYLQGIE				
CRY3BA:	SKGVKTELTRDIFTDPIFTLNALQEYGPTFSSIENSIRKPHLFDYLRGIE				
CRY3A:	PKEVKTELTRDVLTDPIVGVNNLRGYGTTSFSNIENYIRKPHLFDYLAHQ ++++++ ++++++ +++++ +++++ +++++ +++++ +++++ +++++				
	350	360	370	380	390
CRY3C:	FHSRLQPGYFGTDSFNYWSGNVSTRSSIGSDEIIIRSPFYGNKSTLDVQN				
CRY3BB2:	FHTRLQPGYSGKDSFNYWSGNVETRPSIGSSKTITSPFYGDKSTEPVQK				
CRY3BB:	FHTRLQPGYFGKDSFNYWSGNVETRPSIGSSKTITSPFYGDKSTEPVQK				
CRY3BA:	FHTRLRPGYSGKDSFNYWSGNVETRPSIGSNDTITSPFYGDKSIEPIQK				
CRY3A:	FHTRFQPGYYGNDSFNYWSGNVSTRPSIGSNDIITSPFYGNKSSEPVQN ++++++ +++++ +++++ +++++ +++++ +++++ +++++ +++++				
	400	410	420	430	
CRY3C:	LEFNGEKVFRAVANGNLAVWPVGTGGTKIHSGVTKVQFSQYNDRKDEVRT				
CRY3BB2:	LSFDGQKVYRTIANTDVAAPNG----KIYFGVTKVDFSQYDDQKNETST				
CRY3BB:	LSFDGQKVYRTIANTDVAAPNG----KVYLGVTKVDFSQYDDQKNETST				
CRY3BA:	LSFDGQKVYRTIANTDIAAFPDG----KIYFGVTKVDFSQYDDQKNETST				
CRY3A:	LEFNGEKVYRAVANTNLAVWPSA----VYSGVTKVEFSQYNDQTDEAST +++ +++++++ +++++ +++++ +++++ +++++ +++++ +++++				

FIG. 17B

	440	450	460	470	480
CRY3C:	QTYDSKRNVGGIV-FDSIDQLPPIITDESLEKAYSHQLNYVRCFLLQGGR				
CRY3BB2:	QTYDSKRNNNGHVGQAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR				
CRY3BB:	QTYDSKRNNNGHVSQAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR				
CRY3BA:	QTYDSKRYNGYLGQAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR				
CRY3A:	QTYDSKRNVGAVS-WDSIDQLPPIITDEPLEKGYSQVAGPRFTGG +++++ ++++++ ++++++				
	490	500	510	520	530
CRY3C:	GIIPVFTWTHKSVDFYNTLDSEKITQIPFVKAFILVNSTSVVAGPGFTGG				
CRY3BB2:	GTIPFFTWTHERSVDFNNTIDAEEKITQLPVVKAYALSSGASIIEGPGFTGG				
CRY3BB:	GTIPFFTWTHERSVDFNNTIDAEEKITQLPVVKAYALSSGASIIEGPGFTGG				
CRY3BA:	GTIPFFTWTHERSVDFNNTIDAEEKITQLPVVKAYALSSGASIIEGPGFTGG				
CRY3A:	GTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGG ++++++ ++++++ ++++ ++++++				
	540	550	560	570	580
CRY3C:	DII-KCT-NGSLTLYVTPAPDLTYSKTYKIRIRYASTSQVRFGIDLGSY				
CRY3BB2:	NLLFLKESSNSIAFKKVTL-NSAALLQRYRVRIRYASTTNLRLFVQNSNN				
CRY3BB:	NLLFLKESSNSIAFKKVTL-NSAALLQRYRVRIRYASTTNLRLFVQNSNN				
CRY3BA:	NLLFLKESSNSIAFKKVTL-NSAALLQRYRVRIRYASTTNLRLFVQNSNN				
CRY3A:	DII-QCTENGSAATIYVTPD--VSYSQKYRARIHYASTSQITFTLSLDGA +++++ +++++++ ++++++++ ++++++				
	590	600	610	620	630
CRY3C:	THSISYFDKTMDKGNTLTYNFSNLSSVSRPIEISG-GNKIGVSVGGIGSG				
CRY3BB2:	DFIVIYINKTMNIDDDLTQTFDLATTNSNMGFSGDTNELIIGAESFVSN				
CRY3BB:	DFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSN				
CRY3BA:	DFLVIYINKTMNIDGDLTYQTFDFATSNSNMGFSGDTNDFIIGAESFVSN				
CRY3A:	PFNQYYFDKTINKGDTLTYNFSNLASFSTPFELSG--NNLQIGVTGLSAG ++++++ ++++++ ++++ +++++++				
	640	650			
CRY3C:	DEVYIDKIEFIPMD (SEQ ID NO:109)				
CRY3BB2:	EKIYIDKIEFIPVQL (SEQ ID NO:110)				
CRY3BB:	EKIYIDKIEFIPVQL (SEQ ID NO:111)				
CRY3BA:	EKIYIDKIEFIPVQ (SEQ ID NO:112)				
CRY3A:	DKVYIDKIEFIPVN (SEQ ID NO:113)				
	++++++				